

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 13:48:03 ; Search time 6978.47 Seconds

(without alignments)
11880.962 Million cell updates/sec

Title: US-08-153-397A-1

Copyright score: 3962

Sequence: 1 CGGGCCTGAGACTGGGTGA.....AAAAAAACCGGAATT 3962

Scoring table: IDENTITY_NUC

Gappen 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Sequence: 1 CGGGCCTGAGACTGGGTGA.....AAAAAAACCGGAATT 3962
Total number of hits satisfying chosen parameters: 3595312
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: *

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2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

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8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_pat:*

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31: em_htg_other:*

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SUMMARIES

Result No. Score Match Length DB ID Description

1 3962 100.0 3962; DB 6; Length 3962;

2 3675.5 91.5 3754 6 A2378 Sequence 1

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4 3613.4 91.2 3849 9 BC008716 Homo sapi BC013400 Homo sapi

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6 3544.4 89.5 3803 9 HMRTRK L20817 Homo sapi

7 3451 87.1 3637 6 AR094160 Sequence

8 3451 87.1 3637 6 AR103004 Sequence

9 3451 87.1 3637 6 AR105288 Sequence

10 3451 87.1 3637 6 AR105288 Sequence

11 383.2 85.4 3554 6 AX268594 Sequence

12 3383.2 85.4 3554 9 HS7RKE X74979 H_sapiens T

13 3366 85.0 3841 9 HSRETYKL 229993 H_sapiens E

14 312.4 83.6 3692 9 HOMCNA L57508 Homo sapi

15 2105.6 60.7 3659 10 AF026539 Mus musculi AF062595 Mus musculi

16 238.4 60.0 3674 10 MUSCAK L57509 Mus musculi

17 2378 60.0 3743 10 RMTPK3D L26525 Rattus norvegicus AR094162 Sequence

18 1192.2 30.1 1197 6 AR103006 Sequence

19 1192.2 30.1 1197 6 AR105290 Sequence

20 1192.2 30.1 1197 6 AR105290 Sequence

21 1192.2 30.1 1197 6 AR0847 Sequence

22 1010.4 25.5 112018 9 AB023050 AB023050 Homo sapi

23 1010.4 25.5 112018 9 HS7RKL7 AB023050 Homo sapi

24 1010.4 25.5 182207 2 AL66930 HOMO sapi

25 1010.4 25.5 200000 9 AP00511 HOMO sapi

26 1008.8 25.5 48731 9 AC004211 HOMO sapi

27 1008.8 25.5 156384 2 AL62854 Homo sapi

28 991.4 25.0 1072 9 MNTYR010 HSU48705 X90334 H_sapiens g

29 950 24.0 12010 9 U48705 AL62854 Homo sapi

30 642 16.2 3096 9 HSRPKR X7464 H_sapiens m

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32 642 16.2 3157 6 168740 Sequence 4

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34 639.8 16.1 3120 6 AR05640 Sequence

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36 639.8 15.1 3259 11 G49388 G49388 Sequence

37 632.8 16.0 2521 10 AF339455 Cricetulus

38 608.2 15.4 349980 6 AX344571 Sequence

39 572 14.4 660 10 S77855 Ptk-3L-rad1

40 535.4 13.5 349980 6 AX344553 Sequence

41 522.8 13.5 563 6 AX260854 Sequence

42 394 9.9 400 11 G11900 G11900 Sequence

43 362.4 9.1 175345 2 AC023301 Mus musculus

44 362.4 9.1 203476 10 AC071150 Mus musculus

45 341.6 8.6 549 10 S77556 Ptk-3S-rad1

ALIGNMENTS

RESULT 1
168738 LOCUS 168738
DEFINITION Sequence 1 from patent US 5677144. DNA
ACCESSION 168738
VERSION 168738.1 GI:283080
KEYWORDS
SOURCE
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3962)
AUTHORS Ulrich,A. and Alves,F.Hildegarde.Elisabeth.
TITLE Recombinant DNA encoding CCK2, a receptor tyrosine kinase
PATENT US 5677144-A 11-OCT-1997;
JOURNAL
FEATURES Location/Qualifiers
source 1. 3962 /organism="unknown"
BASE COUNT 735 a 1234 c 1182 g 811 t
ORIGIN
Query Match 10.0%; Score 3962; DB 6; Length 3962;
Best Local Similarity 100.0%; Pred. No. 0;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT

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 ACCESSION A42378
 VERSION A42378.1 GI:2297854
 KEYWORDS
 SOURCE
 ORGANISM unidentified
 unclassified.

REFERENCE

1 (bases 1 to 3754)

AUTHORS Gusterson, B.A., Crompton, M.R., Mitchell, P.J., Barker, K.T.,
 Martindale, J.E., Page, M.J. and Spence, P.

TITLE CELL GROWTH FACTOR RECEPTORS
 JOURNAL CANCER RES INST (GB)

COMMENT Other publication AU 7081094 950205.

FEATURES Source

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BASE COUNT
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712

a

c

g

t

712

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RESULT	3	HUMRTR	HUMRTR
DEFINITION	Homo sapiens receptor tyrosine kinase mRNA, complete cds.	3738 bp	mRNA, linear
ACCESSION	L11315.1	GI:03386	
KEYWORDS	receptor tyrosine kinase.		
SOURCE	Homo sapiens (library: lambda-gt1) term placenta cDNA to mRNA.		
ORGANISM	Homo sapiens		

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	I (bases 1 to 3738)
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
COMMENT	On Sep 27, 1993 this sequence version replaced 91:307397.
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RESULT 4

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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3849)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgbps-help@mail.nih.gov
 Tissue Procurement: ARCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NSIC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nigri.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Buffard, G.S., Brinkley, C., Brooks, S.,
 Dietrich, N.I., Guan, X., Gupta, J., Ho, S.-L., Karins, E., Legaspi, R.,
 Llin, M., Madiro, O., Masiello, S., Mastrangelo, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stanton, P.S., Thomas, P.J.,
 Thompson, E.B., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINNt att: <http://Image.lnl.gov>

Series: IML Plate: 1 Row: 0 Column: 24
 This clone was selected for full length sequencing because it
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Location/Qualifiers

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CDS

BASE COUNT 715 a 1181 c 1165 g 788 t
 ORIGIN

Query Match 91.2%; Score 3613.4; DB 9; Length 3849;
 Best Local Similarity 95.9%; Pred. No. 0; Mismatches 31; Index 130; Gaps 3;
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Qy	1682	GTGGAGAGGAGCTGAGGGTCACTCTGTCCTGGGAGACTATCCATCACAA	1741	Db	2655	CTGGATGCTGGGAGGAGCTCATCTCATGAGGAGCT	2714
Db	1704	GTGGAGAGGAGCTGAGGGTCACTCTGTCCTGGGAGACTATCCATCACAA	1763	Qy	2882	CACCGAGGAGGAGCTGAGGAGGAGCT	2941
Qy	1742	CGGCCAGGTCTAGAGAGCACCCCGTACAGGGGCCCTGGAGAATCGCC	1801	Db	2822	CTTGGTCTGACCTCTGCTGAGGAGCT	2881
Db	1764	CGGCCAGGTCTAGAGAGCACCCCGTACAGGGGCCCTGGAGAATCGCC	1823	Qy	2775	CACCGAGGAGGAGCTGAGGAGGAGCT	2834
Qy	1802	CGACCTGGCTGGCTGGGAGGAGCTGAGGAGGAGCT	1861	Qy	2942	GTACCTGGGAGGAGGAGCTGAGGAGGAGCT	3001
Db	1824	CGACCTGGCTGGCTGGGAGGAGCT	1854	Db	2835	GTACCTGGGAGGAGCTGAGGAGGAGCT	2894
Db	1855	--	1854				

QY	3790	GTGCCACATGAGTTTCTATACCTTGGGTTGACATTGAGGGAGACAA	3849
Db	3631	GTGCCACATGAGTTTCTATACCTTGGGTTGACATTGAGGGAGACAA	3690
QY	3850	CAGATTTACCTAAATATGACCCPAGCTTGAGGCAATTAACTCCCTGACTAGG	3909
Db	3691	CAGA-TTITACCTAAATATGACCCPAGCTTGAGGCAATTAACTCCCTGACTAGG	3748
QY	3910	AGTAATATAAAGGTGAGTTCCACAAAAA	3953
Db	3749	AGTAATATAAATGTGAGTTCCACAAAAA	3792
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LOCUS	AR094160	3637 bp	DNA linear
DEFINITION	Sequence 3 from patent US 6001621.	PAT	08-SEP-2000
ACCESSION	AR094160		
VERSION	AR094160.1	GR:10020905	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 3637)		
AUTHORS	Godowski, P.J., Mark, M.R. and Scadden, D.T.		
TITLE	Protein tyrosine kinases		
JOURNAL	Patent: US 6001621-A 3 14-DEC-1999;		
FEATURES	1. 3637 /organism="unknown"		
source			
BASE COUNT	721 a 1094 c 1079 g 743 t		
ORIGIN			
Query Match	87.1%	Score 3451	DB 6; Length 3637;
Best Local Similarity	97.0%	Pred. No. 0;	Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;
QY	256	GTGGACTGAGGAATGCAAGAGATGCTGCCACCCCTTAGGCCAGGGATCAG	315
Db	17	GTGGACTGAGGAATGCCAGAGATGCTGCCACCCCTTAGGCCAGGGATCAG	76
QY	316	GAGCTATGGACCAAGGCCCTGTCATCTTAAGCTCTGCGCTCTGGCAAGTGG	375
Db	77	GAGCTATGGACCAAGGCCCTGTCATCTTAAGCTCTGCGCTCTGGCAAGTGG	136
QY	376	ATGCTGACATGAGGACATTTGATCCCTGCCAATGCCCTATGCCCTGGCAGTCAG	435
Db	137	ATGCTGACATGAGGACATTTGATCCCTGCCAATGCCCTATGCCCTGGCAGTCAG	196
QY	436	ACCGGACCATCCAGACAGAGACATCTGCTCCAGCTCTGGCAGATTCACGTGG	495
Db	197	ACCGGACCATCCAGACAGCTCTGCTCCAGCTCTGGCAGATTCACGTGG	256
QY	496	CCCGCACACAGCAGGTTGGAGACGACTGAGGGATGGGCTGTGCCCGAGGTGG	555
Db	257	CCCGCACACAGCAGGTTGGAGACGACTGAGGGATGGGCTGTGCCCGAGGTGG	316
QY	556	TGTTTCCCAAGGAGGAGGAGGACTCTGAGGGATCTACACGACTCCACCTGGGCTGTGCCCGAGGTGG	615
Db	317	TGTTTCCCAAGGAGGAGGACTCTGAGGGATCTACACGACTCCACCTGGGCTGTGCCCGAGGTGG	376
QY	616	TGGGGGACCCAGGGCGCAGCGCCGGCGCGAGGACTCTCCGGAGCTAC	675
Db	377	TGGGGGACCCAGGGCGCAGCGCCGGCGCGAGGACTCTCCGGAGCTAC	436
QY	676	GGCTGCGTTACTCCGGGATGTCGCCCTGGATGGCTGAGGACCCGGCTGGTCAG	735
Db	437	GGCTGCGTTACTCCGGGATGTCGCCCTGGATGGCTGAGGACCCGGCTGGTCAG	496
QY	736	AGGTGATCTAGGACATGAGGACCTGAGGAGGAGGCTGAGGACCCGGCTGGCCCA	795
QY	796	TGTTTCCGGACTCTCTGCCCCGGAGACTCTCCAGACATCAACAGCCAGGCTA	1755
Db	557	TGTTTCCGGACTCTCTGCCCCGGAGACTCTCCAGACATCAACAGCCAGGCTA	616
QY	856	GGCTGAGCTATGCTGCCCTGGAGGATGAGCTCTCAACGCCCTGCTG	915
Db	617	GGCTGAGCTATGCTGCCCTGGAGGATGAGCTCTCAACGCCCTGCTG	676
QY	916	GGAGACAATGTTACTCTGAGGCTGAGCTCCACCTAGACGACATA	975
Db	677	GGCAGACATGTTACTCTGAGGCTGAGCTCCACCTAGACGACATA	736
QY	976	CGCTGCGGGAGTGCAGTGGGCTCTGGCCACSTGGCGATGCTGCTGCTG	1035
Db	737	CGCTGCGGGAGTGCAGTGGGCTCTGGCCACSTGGCGATGCTGCTGCTG	795
QY	1036	ATGACTTTAGGAGACTCAGGAGCTGGGCTGGGCTGGCAGGTATGACTATG	1095
Db	797	ATGACTTTAGGAGACTCAGGAGCTGGGCTGGGCTGGCAGGTATGACTATG	915
QY	1096	GGACACAGCTCTCAGGAGCTGGGATGGAGATGGAGTGGATGAGTTGAC	856
Db	857	GGACACAGCTCTCAGGAGCTGGGATGGAGTGGATGAGTTGAC	916
QY	1156	CCTTCCAGGTATGCCGACTGTCAGTGGACACATGCGCTGGGCCCTG	1215
Db	917	CCTTCCAGGTATGCCGACTGTCAGTGGACACATGCGCTGGGCCCTG	976
QY	1216	GGGGGGGAGATGTCCTCGGGGGGGCCCTGCCATGGCGCTGGGAGGGAG	1275
Db	977	GGGGGGGAGATGTCCTCGGGGGGGCCCTGCCATGGCGCTGGGAGGGAG	1036
QY	1276	GGCACACCTAGGGGCAACCTGGGAGCCAGGGCCAGAGCCGGGCTG	1335
Db	1037	GGCACACCTAGGGGCAACCTGGGAGCCAGGGCCAGGCGGGCTG	1096
QY	1336	GGGGCGGTGGCTGCTCTGAGCTGGCGCTCTCTCTGAGCTGGCTACT	1395
Db	1097	GGGGCGGTGGCTGCTCTGAGCTGGCGCTCTCTCTGAGCTGGCTACT	1156
QY	1396	TCAGGCAATCTCTCACTCTGAGTGTGGTAAGAACATCCTCTGGGACTGAG	1455
Db	1157	TCAGGCAATCTCTCACTCTGAGTGTGGTAAGAACATCCTCTGGGACTGAG	1216
QY	1456	CCTTCCGGCCAGCCCTGGGGCCACCTCCACACCTCCACACTGGAGGCA	1515
Db	1217	CCTTCCGGCCAGCCCTGGGGCCACCTCCACACCTCCACACTGGAGGCA	1276
QY	1516	AGCTGGAGGCCAGGGCCAGCAGCCGGCTGGCAAGGGAGGGAGGCCATCC	1575
Db	1277	AGCTGGAGGCCAGGGCCAGCAGCCGGCTGGCAAGGGAGGGAGGCCATCC	1336
QY	1576	TCATGGCTCTCTGGGCAATCATCTCTCTCTGCTCATCATCTGGCT	1635
Db	1337	TCATGGCTCTCTGGGCAATCATCTCTCTCTGCTCATCATCTGGCT	1396
QY	1636	GGCGCGCTGACTGGCCAGCTCTGAGGTGGAGGAGGCTGGAGGAGGAGC	1695
Db	1397	GGCGCGCTGACTGGCCAGCTCTGAGGTGGAGGAGGAGGAGGAGC	1456
QY	1696	TGACGGTCACTCTCTGCCCCGGAGACTCTCCAGACATCAACAGCCAGGCTA	1755
Db	1457	TGACGGTCACTCTCTGCCCCGGAGACTCTCCAGACATCAACAGCCAGGCTA	1516
QY	1756	GAGGCCACCCCTACAGGAGCCAGCTCTGAGGTGGAGGAGGAGGAGC	1815
Db	1517	GAGGCCACCCCTACAGGAGCCAGCTCTGAGGTGGAGGAGGAGGAGC	1576
QY	1816	GTGCGCCAAATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGC	1875
Db	1577	GTGCGCCAAATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGC	1636

QY	1876	CTTACCCCGTCCCCCTCGAGGGGGCCCCCACCGCCCTGGGCCAACCCACCA	1935	QY	2956	CGCTTCCCCTCCCGAGGSCCTATATGAGCTGATCTGGCTGGCTGGAGCTG	3015	
Db	1637	CTTACGGCCGTCGCCCTCGAGGCCGGGCCACACCGCCTGGGCCAACCCACCA	1996	Db	2699	CGCCPCCGCTCCCGAGGSCCTATATGAGCTGATCTGGCTGGCTGGAGCTG	2758	
QY	1936	ACACCCAGGGCTACAGTGGGACATATGAGGCTGAGAGACGCAAGGCCCTCTGC	1995	QY	3016	AGCACCGACACCCCTTCCAGCTGATCTGGCTGGCTGGAGCTGACTCACACCG	3075	
Db	1697	ACACCCAGGGCTACAGTGGGACATATGAGGCTGAGAGACGCAAGGCCCTCTGC	1756	Db	2759	AGCACCGACACCCCTTCCAGCTGATCTGGCTGGCTGGAGCTGACTCACACCG	2818	
QY	1996	CCCCACCTCCAGAAGACAGCTGGGACATATGAGGCTGAGAGACGCAAGGCCCTCTGC	2055	QY	3076	TGTGATCACACATCCAGCTGAGCTGGCTCTGGCTGAGCTGAGCTGAGCA	3135	
Db	1757	CCCCACCTCCAGAAGACAGCTGGGACATATGAGGCTGAGAGACGCAAGGCCCTCTGC	1916	Db	2819	TGIGATCACACATCCAGCTGAGCTGGCTCTGGCTGAGCTGAGCTGAGCA	2878	
QY	2056	GGTGTACCCGGGCAACACCTATCTGCTGCTGACTGCCCCATATGAGGCTGAGCTGGGATG	2115	QY	3135	CTAACACAGAGGACACATGGCAACCTCTGCCCCCTCCCTCCAGACAGGCCATACCT	3195	
Db	1817	GGTGTACCCGGGCAACACCTATCTGCTGCTGACTGCCCCATATGAGGCTGAGCTGGGATG	1876	Db	2879	CTAACACAGAGGACACATGGCAACCTCTGCCCCCTCCCTCCAGACAGGCCATACCT	2938	
QY	2116	GGCCCCCAGAGTGGATTCCTCGATCTGAGTCAAGGAGAGCTGGGAG	2175	QY	3196	AATAGAGGAGTGGAGCTGGGGCTGGGCCACCCAGGGAGCTGAGCTGAGCA	3255	
Db	1877	GGCCCCCAGAGTGGATTCCTCGATCTGAGTCAAGGAGAGCTGGGAG	1936	Db	2939	AATAGAGGAGTGGAGACTC-----	2958	
QY	2176	GCACAGTTGGGAGGTGACCTCTGAGCTGAGCTGAGCTGAGCTGGGAG	2235	QY	3256	CCCTTCTGACACACTCTCATGTCCTCTCCCTCCAGGGAGCTGAGCTGAGCA	3315	
Db	1937	GCACAGTTGGGAGGTGACCTCTGAGCTGAGCTGAGCTGAGCTGGGAG	1996	Db	2959	-----	AGAGCCCTGTG	2972
QY	2236	ATTTCCCCCTTAATGTCGTAAGGACACCTTGTGTTAGCTGTCAGATCTACGC	2295	QY	3316	CCACCCACACTGGCTGGAGCTCTCCACCTCTCTAGGATCCCTTGGG	3375	
Db	1997	ATTTCCCCCTTAATGTCGTAAGGACACCTTGTGTTAGCTGTCAGATCTACGC	2056	Db	2973	CCACCCACACTGGCTGGAGCTCTCCACCTCTAGGATCCCTTGGG	3032	
QY	2296	CAGATGCCACCAAGAATGCCAGCTCTCTGTCAGGAAATGATTCCTGAGG	2355	QY	3376	AAGGGGGAGAAATATGGATAGACAGCTGGACATGGCATGGGACCTGGGCC	3435	
Db	2057	CAGATGCCACCAAGAATGCCAGCTCTCTGTCAGGAAATGATTCCTGAGG	2098	Db	3033	AAGGGGGAGAAATATGGATAGACAGCTGGACATGGCATGGGACCTGGGCC	3092	
QY	2356	TGAAAGATCATGTCAGGCTCAAGGACCCACATCATGGCTGAGTGGTC	2415	QY	3436	ACTGGACACACATGATCTGGAGAGTGGCTGAGCTGGCTGAGTGGTC	3494	
Db	2099	TGAAAGATCATGTCAGGCTCAAGGACCCACATCATGGCTGAGTGGTC	2158	Db	3093	ACTGGACACACATGATCTGGAGAGGAGCTGGCCCTGGCCAGCTGTC	3152	
QY	2416	AGGAGGACCCCTCTGCAATGATGACTGACTACATGGAGACGSCGACTCAACAGTTC	2475	QY	3495	ACATGGACACCCACTGGCTGGAGATCTGGGGAGGGAGACAGAAGGAGGAATG	3554	
Db	2159	AGGAGGACCCCTCTGCAATGATGACTGACTACATGGAGACGSCGACTCAACAGTTC	2218	Db	3153	ACATGGACACCCACTGGCTGGAGATCTGGGGAGGGAGACAGAAGGAGGAATG	3212	
QY	2476	TCACTGCCACCAACTGGGAGGACAGGGAGGCCAGGGGCCCTGGGACGGCAGGTG	2535	QY	3555	TTCTCTGGCCCTCTCTGACTCTGTCAGCTGGCTCTCCCTCCATCACCT	3614	
Db	2219	TCACTGCCACCAACTGGGAGGACAGGGAGGCCAGGGGCCCTGGGACGGCAGGTG	2278	Db	3213	TTCTCTGGCCCTCTCTGACTCTGTCAGCTGGCTCTCCCTCCATCACCT	3272	
QY	2536	CGCAGGGGCCACCATCACGCTACGCCAATCTGGTCACTGGCATGGGAGGAGATG	2595	QY	3615	GAACACTGGACCTGGGGTAGGCCAGGGCCACTCCCTGGCTCTCCCTCC	3674	
Db	2279	CGCAGGGGCCACCATCACGCTACGCCAATCTGGCATGGCATGGGAGGAGATG	2338	Db	3273	GAACACTGGACCTGGGGTAGGCCAGGGCCACTCCCTGGCTCTCCCTCC	3332	
QY	2596	GCATGCGCTATCTGCGCACACTGACTCTGGTACATCGGACCTGGCCACGCTG	2655	QY	3675	CAGCTGGAGCTGAGACTCTCTAAGGCTATAGCTTGTGGAGTAATATGGGT	3734	
Db	2339	GCATGCGCTATCTGCGCACACTGACTCTGGTACATCGGACCTGGCCACGCTG	2398	Db	3333	CAGCTGGAGCTGAGACTCTCTAAGGCTATAGCTTGTGGAGTAATATGGGT	3392	
QY	2656	TAGTGGGAAATTCAACCATCAAATGCCAGACTTGGCATGGGAGCTCTCTG	2715	QY	3735	GGGGGAAGAGGGAGCAAGGCCATAGGCCCTGGGTGGCATCTAGCTGAGCTG	3794	
Db	2399	TAGTGGGAAATTCAACCATCAAATGCCAGACTTGGCATGGGAGCTCTCTG	2458	Db	3393	GGGGGAAGAGGGAGCAAGGCCATAGGCCCTGGGTGGCATCTAGCTGAGCTG	3452	
QY	2776	CTGGGACTATACCGTGTGCGAGGTGTACGACTGCGGTGAGCTGGCTGGCTGG	2835	QY	3795	CACATGTTCTATACCTGGGTGTACCTGGCATCTGGGTGGAGACAGAT	3854	
Db	2519	CTGGGACTATACCGTGTGCGAGGTGTACGACTGCGGTGAGCTGGCTGGCTGG	2775	Db	3453	CACATGTTCTATACCTGGGTGTACCTGGGTGGCATCTGGGTGGAGACAGAT	3512	
QY	2836	TGGGGAGTGTGAGTGTGAGGTGTACGACTGCGGTGAGCTGGCTGGCTGG	2895	QY	3855	TTTACACTATATGGACCTAGCTGGCATCTGGGTGGCATCTAGCTGAGCTG	3914	
Db	2579	TGGGGAGTGTGAGGTGTACGACTGCGGTGAGCTGGCTGGCTGGCTGG	2638	Db	3513	TTTACACTATATGGACCTAGCTGGCATCTGGGTGGCATCTGGGTGGAGACAGAT	3572	
QY	2896	TCTCGAGAACGGGGGAGTGTCTCGGAGCAGGGCCAGGGCCAGGGCTGG	2955	QY	3915	ATATAAAGGTGAGTTTCCACAAAAAA	3953	
Db	2639	TCTCGAGAACGGGGGAGTGTCTCGGAGCAGGGCCAGGGCTGG	2698	Db	3573	ATATAAAGGTGAGTTTCCACAAAAAA	3611	

RESULT 8

AR103004

LOCUS AR103004

DEFINITION Sequence 3 from patent US 6087144.

3637 bp DNA

Linear

PAT 14-FEB-2001

ACCESSION	REFERENCE	KEYWORD	AR103004.1	GI:12814592
		SOURCE	Unknown.	
		ORGANISM	Unclassified.	
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	Scadden, D. T., Baker, K. P. and Baron, W. F.	AUTHORS		
	Protein tyrosine kinases	TITLE		
	Patent: US 608144-A 3 11-JUL-2000;	JOURNAL		
	Location/Qualifiers	FEATURES		
	1. .3637	Source	/organism="unknown"	
BASE COUNT	721	a	1094	c
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Matches	3589;	Conservative	0;	Mismatches
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QY	256	GGTGGACTTGGAGGAAATGCCAAGAGATGCTGCCCCACCCCTAGGCCGAGGATCAG	315	
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QY	316	GAGCTATGGACCAAGGGCCCTGTCATCTTACTGCTCTGCTCTGGCAAGTGGAG	375	
Db	77	GAGCTATGGACCAAGGGCCCTGTCATCTTACTGCTCTGCTCTGGCAAGTGGAG	136	
QY	376	ATGCTGACATGAGGGACATTTGATCCTGCCAGTGCCTGGCATGCGCAG	435	
Db	137	ATGCTGACATGAGGGACATTTGATCCTGCCAGTGCCTGGCATGCGCAG	196	
QY	436	ACGGACCATCCAGACAGTACATCTCTGCTCCAGCTCTGGTCAAGTCAC TGCG	495	
Db	197	ACGGACCATCCAGACAGTACATCTCTGCTCCAGCTCTGGTCAAGTCAC TGCG	256	
QY	496	CCGCACAGACAGGTTGAGACAGCTGACGGGGATGGGGCTGGCCCGAGGGTGG	555	
Db	257	CCGCACAGACAGGTTGAGACAGCTGACGGGGATGGGGCTGGCCCGAGGGTGG	316	
QY	556	TGTTTCCAAAGGAGGAGGAGTCTCAGGTTGATCTACAACTGCACTGGTC	615	
Db	317	TGTTTCCAAAGGAGGAGTCTCAGGTTGATCTACAACTGCACTGGTC	376	
QY	616	TGGTGGCACCCAGGGACGCGATGGGGGGCTGGCAAGGAGTTCCCGGAGCTAC	675	
Db	377	TGGTGGCACCCAGGGACGCGATGGGGGGCTGGCAAGGAGTTCCCGGAGCTAC	436	
QY	676	GGCTCGTACTCTCCGGATGTCGCGCTCTGGATGGGGCTGGAGGCTCAG	735	
Db	437	GGCTCGTACTCTCCGGATGTCGCGCTCTGGATGGGGCTGGAGGCTCAG	496	
QY	736	AGGGATCTAGGCATGAGACGACCTGGAGGAGTGTGAGGACTTGGGCCCC	795	
Db	497	AGGGATCTAGGCATGAGACGACCTGGAGGAGTGTGAGGACTTGGGCCCC	436	
QY	796	TGGTGGCCACTGGTCGTTCTACCCCGGCTGACGGGTCTGGGCTGAGGACCT	556	
Db	557	TGGTGGCCACTGGTCGTTCTACCCCGGCTGACGGGTCTGGGCTGAGGACCT	616	
QY	856	GGGTAGACTCTATGCTGCTCTGGAGGATGGACTCCGCTCTACACGCCCTCTG	915	
Db	617	GGGTAGACTCTATGCTGCTCTGGAGGATGGACTCCGCTCTACACGCCCTCTG	676	
QY	916	GGCAGACATGTTATCTGAGGGCTGACTCTAGGACTCCACCTATGAGGACATA	975	
Db	677	GGCAGACATGTTATCTGAGGGCTGACTCTAGGACTCCACCTATGAGGACATA	736	
QY	976	CCGGGGGACTGCACTGGAGGATGGGTCTGGCCAGTGGGCTCTGGGCTG	1035	
Db	737	CCGGGGGACTGCACTGGAGGATGGGTCTGGCCAGTGGGCTCTGGGCTG	796	
QY	1036	ATGACTTAAAGAAGTCAGGAGCTGGCGGATCTGGCGCTGAGCTATGTTGATG	1095	
Db	797	ATGACTTAAAGAAGTCAGGAGCTGGCGCTGCGCTGAGCTATGTTGATG	856	
QY	1096	GCACACAGCTTCCAGTGTGAGGATGGCTGCGCTGCGCTGAGCTATGTTGATG	1155	
Db	857	GCACACAGCTTCCAGTGTGAGGATGGCTGCGCTGCGCTGAGCTATGTTGATG	916	
QY	1156	CTTCCAGCTATGCAAGTGTGAGGATGGCTGCGCTGCGCTGAGCTATGTTGATG	1215	
Db	917	CTTCCAGCTATGCAAGTGTGAGGATGGCTGCGCTGCGCTGAGCTATGTTGATG	976	
QY	1216	GGGGGGTGAATGCTGCTTCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1275	
Db	977	GGGGGGTGAATGCTGCTTCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1036	
QY	1276	GCCACACCTAGGGGAACTGGGGAACTGGGGAACTGGGGGGGGGGGGGGGGGG	1335	
Db	1037	GCCACACCTAGGGGAACTGGGGAACTGGGGGGGGGGGGGGGGGGGGGGGGGG	1096	
QY	1336	GGGGGGCTGTGGCTCTGGCTCTGGCTCTGGCTCTGGGGGGCTGTGTACTCT	1395	
Db	1097	GGGGGGCTGTGGCTCTGGCTCTGGCTCTGGGGGGCTGTGTACTCT	1156	
QY	1396	TCAGCGAAATCCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1455	
Db	1157	TCAGCGAAATCCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1216	
QY	1456	CCTTCGGCCAGCCCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1515	
Db	1217	CCTTCGGCCAGCCCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1276	
QY	1516	AGCTGGACGCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1575	
Db	1277	AGCTGGACGCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1336	
QY	1576	TCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1635	
Db	1337	TCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1396	
QY	1636	GGCGGTGCACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1695	
Db	1397	GGCGGTGCACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1456	
QY	1696	TGACGTTCACTCTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTG	1755	
Db	1457	TGACGTTCACTCTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTG	1516	
QY	1756	GAGACCCGG	1815	
Db	1517	GAGACCCGG	1576	
QY	1816	GTGTCCTCAATGGCTCTGGGTGCTCTCTCCATCACTGACGACGCCAG	1875	
Db	1577	GTGTCCTCAATGGCTCTGGGTGCTCTCTCCATCACTGACGACGCCAG	1636	
QY	1876	CTTAGCCCCCTGAGGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1935	
Db	1637	CTTAGCCCCCTGAGGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1696	
QY	1936	ACACCCGGCTACAGTGTGGGACTATATGGGGCTGGAGGCTGGGGGGGG	1995	
Db	1697	ACACCCGGCTACAGTGTGGGACTATATGGGGCTGGAGGCTGGGGGG	1816	
QY	1996	CCCCACCTCCAGACAGGGCTCCACCATATGGGGCTGGAGGCTGGGGGG	2055	
Db	1757	CCCCACCTCCAGACAGGGCTCCACCATATGGGGCTGGAGGCTGGGGGG	1755	
QY	2056	GGGTCACCGGGGGCAACACCTATGCTGCTGCTGCTGCTGCTGCTG	2115	
Db	1817	GGGTCACCGGGGGCAACACCTATGCTGCTGCTGCTGCTGCTGCTG	1876	

Db	1877	GGCCCCCAGACTGGATTCCCTCGATCTCGACTCCCTCTCAAGGAGAACCTGGGAGG	1936	Db	2939	AATAGAGGCGTGTGAGCTG-----	2956
Qy	2176	GGCGATTTGGGAGGTGTCACCTCCACCTGTTGAGGTGAGCACACCTCTCAAGATCTGGTCAGTCAGTTG	2235	Qy	3256	CCCTTCTGAGACACHTCTCATGNCCTTCTGTCTTCCTCTAGAAGCCCTGTGCG	3315
Db	1937	GGCAGTTGGGAGGTGCACTCTGAGGAGGAGCTCAAGATCTGGTCAGTCAGATCTGGTCAGTC	1996	Db	2959	-----AGAGCCCTGTGCG	2972
Qy	2236	ATTCCTCCCTTAATGTCGCTAAGGGCACCCCTTGCGTGTCTGTCAGATCTTACGGC	2295	Qy	3316	CCACCCAGCTGCTCTGTTGATGCTCACCCTCTAGCCCTCTAGCCCTCTGGG	3375
Db	1997	ATTCCTCCCTTATGTCGCTAAGGGACACCTTGTGTTAGTCAGATCTTACGGC	2056	Db	2973	CCACCCAGCTGCTCTGTTGATGCTCACCCTCTAGCCATCCCTCTGGG	3032
Qy	2296	CAGATGCCACCAAGATGTCAGCTCTCCCTGTCAGGATGTTCTGAAGAGG	2355	Qy	3376	AAGGGGGAGANATAAGGATAGACACTGGACATGGACATGGCCATGAGCACCTGGGCC	3435
Db	2099	TGAGATCTATGTCGAGGCTCAAGGACCCAAACATCATCTGGCTCTGGCTG	2158	Db	3033	AASGGTGGAGAAATATGGATAGACACTGGACATGGACATGGCCATGAGCACCTGGGCC	3092
Qy	2416	AGGAGACCCCTCTCATGTTACTGACTACATGGAGGGGGGCTGGGAGGGACCTAACAGTC	2475	Qy	3495	ACATGGACCCACTGGAGAGAATGGGAGCTGGACATGGACATGGCCATGAGGAGAATG	3554
Db	2159	AGGAGACCCCTCTCATGTTACTGACTACATGGAGGGGGCTGGGAGGGAGCTG	2415	Db	3153	ACATGGACCCACTGGAGAGAATGGGAGCTGGACATGGACATGGCCATGAGGAGAATG	3212
Qy	2476	TCACTGCCACCAAGCTGGAGGAQAGGCCAGGGGGGGGCTGGGAGGGAGCTG	2535	Qy	3436	ACTGGACAACACTGATCTGGCTGAGAATCTGGGAGCTGGGAGCTGGGAGCTG	3494
Db	2219	TCACTGCCACCAAGCTGGAGGAQAGGCCAGGGGGGGGCTGGGAGGGAGCTG	2278	Db	3093	ACTGGACAACACTGATCTGGCTGAGGAGGGGGGCTGGGAGGGAGCTG	3152
Qy	2536	CGCGGGGCCACCATCATGCTACCCATGCTGAGGAGGGGGCTGGGAGGGAGCTG	2595	Qy	3555	TTCTTGTGCTCTCTGTTACTGTTGCTCTGAGCTGGGAGCTGGGAGCTGGGAGCTG	3614
Db	2279	CCGAGGGCCACCATCATGCTACCCATGCTGAGGAGGGGGCTGGGAGGGAGCTG	2338	Db	3213	TTCTTGTGCTCTCTGTTACTGTTGCTCTGAGCTGGGAGCTGGGAGCTGGGAGCTG	3272
Qy	2596	GCATGGCTACTGGCACACTCAACTTGTACATGGGACCTGGGACGGGAACTG	2655	Qy	3675	CAGCTTGAGCTGAGACTCTCAAGCTGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTG	3734
Db	2339	GCATGGCTACTGGCACACTCAACTTGTACATGGGACCTGGGACGGGAACTG	2398	Db	3333	CAGCTTGAGCTGAGACTCTCAAGCTGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTG	3392
Qy	2656	TAGTGGGAATTTCACATCAAAATGGAGACTTGGATGAGCCGAACTCTG	2715	Qy	3735	GGGGGAAGAGGGCACAGGCCCTAGCCCTGCTGGGAGCTGGGAGCTGGGAGCTG	3794
Db	2399	TAGTGGGAATTTCACATCAAAATGGAGACTTGTGAGCTGGGAGCTGGGAGCTG	2458	Db	3393	GGGGGAAGAGGGCACAGGCCCTAGCCCTGCTGGGAGCTGGGAGCTGGGAGCTG	3452
Qy	2716	CTGGGGACTATTACCGTGTGAGGGGGGGAGTGTGTCCTCCATCCGGCTGATGGCTGGG	2775	Qy	3795	CACATGATTCTATACACTTGGGTTGTCATTTGGGGAGAGACAGAT	3854
Db	2459	CTGGGGACTATTACCGTGTGAGGGGGAGTGTGTCCTCCATCCGGCTGATGGCTGG	2518	Db	3453	CACATGATTCTATACACTTGGGTTGTCATTTGGGGAGAGACAGAT	3512
Qy	2776	AGTCATCTCATGGGAAGTTCACGACTGGAGTACGCTGGGCTTGTGTC	2835	Qy	3855	TTTACACTAATATGGACTACTTGGCAATTATTCCTGGCTAGGAGTA	3914
Db	2519	AGTCATCTCATGGGAAGTTCACGACTGGAGTACGCTGGGCTTGTGTC	2578	Db	3513	TTTACACTAATATGGACTACTTGGCAATTATTCCTGGCTAGGAGTA	3572
Qy	2836	TGTGGAGGCTGTGCTCTGTAGGCCAGCCCTGGGAGCTCACGAGCAGGAG	2895	Qy	3915	ATATAAAGGTGTTTCCACAAAAAAAGAAAAAA	3953
Db	2579	TGTGGAGGCTGTGCTCTGTAGGCCAGCCCTGGGAGCTCACGAGCAGGAG	2638	Db	3573	ATATAAAGGTGTTTCCACAAAAAAAGAAAAAA	3611
Qy	2896	TCATCGAGAAGGGGGAGATCTCTCGGGGACCAAGGGCCGAGGGTACCTGGTCCGGC	2955	RESULT	9		
Db	2639	TCATCGAGAAGGGGGAGATCTCTCGGGGACCAAGGGCCGAGGGTACCTGTCCGGC	2698	AR105288			
Qy	2956	CGCTCTGCTCCGGCGAGGGCTATAGGAGCTGATCTGCTGCTGAGGGAGCTG	3015	LOCUS	AR105288		
Db	2699	CGCTCTGCTCCGGCGAGGGCTATAGGAGCTGATCTGCTGCTGAGGGAGCTG	2758	DEFINITION	Sequence 3 from patent US 6096557.		
Qy	3016	AGCAGCACCCCTTCCAGTCATGGTCTGGCGAGGGAGCTCAACACGG	3075	ACCESSION	AR105288		
Db	2759	AGCAGCACCCCTTCCAGTCATGGTCTGGCGAGGGAGCTCAACACGG	2818	VERSION	AR105288.1		
Qy	3076	TGTGAACTCAACATCCAGCTCCCTCTCAGGGAGTGTGTCAGGGAGACCCAGTGACA	3135	KEYWORDS	GI:12818885		
Db	2819	TGTGAACTCAACATCCAGCTCCCTCTCAGGGAGTGTGTCAGGGAGACCCAGTGACA	2878	SOURCE	Unknown.		
Qy	3136	CTAAACGAGGAGCACTGACCTCTCCCTCCCTCCAGGGAGTGTGTCAGGGAGACCCAGTGACA	3195	ORGANISM	Unclassified.		
Db	2879	CTAAACGAGGAGCACTGACCTCTCCCTCCCTCCAGGGAGTGTGTCAGGGAGACCCAGTGACA	2938	REFERENCE	1 (bases 1 to 3637)		
Qy	3196	ATAGAGGCGTGTGAGCTGGGGTGGCCACCCAGGGAGCTGAGGCCCTCTC	3255	AUTHORS	Godowski, P.J., Mark, M.R. and Scadden, D.T.		
			TITLE	Nucleic acids encoding protein tyrosine kinases			
			JOURNAL	Patent: US 6096527-A 3 01 AUG-2000;			
			FEATURES	Location/Qualifiers			
			SOURCE	1, 3637			
			BASE COUNT	721 a 1094 c 1079 g 743 t			
			ORIGIN				

Best Local Similarity	97.0%	Pred.	No. 0	Mismatches	Db	1037	GCACACACTTGGGCCAATCTGGGGACCCAGGGGGGCTCTCTAGGCCCTTG
Matches	3589;	Conservative	0;	Indels	5;	105;	Gaps
						3;	
256	GTGACTTGTAGGAATGCCAGAGATGCTCCCTCACCCCTTAGGCCAGGGATCG	Qy	1336	GCACACACTTGGGCCAATCTGGGGACCCAGGGGGGCTCTCTAGGCCCTTG	1395		
17	GTGACTTGTAGGAATGCCAGAGATGCTCCCTCACCCCTTAGGCCAGGGATCG	Db	1097	GCACACACTTGGGCCAATCTGGGGACCCAGGGGGGCTCTCTAGGCCCTTG	1156		
316	GTGACTTGTAGGAATGCCAGAGATGCTCCCTCACCCCTTAGGCCAGGGATCG	Qy	1396	TCAGGAAATCTCTCATCTGATGTTGAGACATCTCTGGACTGGAGGA	1455		
77	GTGACTTGTAGGAATGCCAGAGATGCTCCCTCACCCCTTAGGCCAGGGATCG	Db	1157	TCACGAAATCTCTCATCTGATGTTGAGACATCTCTGGACTGGAGGA	1216		
376	ATGCTGACATGAGGACATTGTGATCTCTGCAGTGGCAAGTGGAAAGTGGAG	Qy	1456	CTTTCGCCAGGCCCTGTGSCCCCTGCCACTCGCCACTGGCATGCGCTTG	1515		
137	ATGCTGACATGAGGACATTGTGATCTCTGCAGTGGCAAGTGGAAAGTGGAG	Db	1217	CCFCCGCCAGGCCCTGTGSCCCCTGCCACTCGCCACTGGCATGCGCTTG	1276		
436	ACCGGACATCCAGCTGAGCTGATCTCTCTTCCAGCTCTGGTCACTCCG	Qy	1515	ACCGGACCCAGGGCCAGCAGGCCAAAGCCAGGGAGGCCACCCATCC	1575		
197	ACCGGACATCCAGCTGAGCTGATCTCTCTGCTTACTGCGCTCTGTGAG	Db	1277	ACCGGACCCAGGGCCAGCAGGCCAAAGCCAGGGAGGCCACCCATCC	1336		
556	TGTTTCCAAGGAGGAGGAGTACTTGAGGGGATCTACAAAGACTCCACCTGGCTC	Qy	1636	GGCGCTGACTCGCAGGCTCTCGCAAGGAGGTGAGGAGGAGGAGGAG	1695		
317	TGTTTCCAAGGAGGAGGAGTACTTGAGGGATCTACAAAGACTCCACCTGGCTC	Db	1397	GGCGCTGACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1456		
616	TGTTTCCAAGGAGGAGGAGTACTTGAGGGATCTACAAAGACTCCACCTGGCTC	Qy	1696	TGACGGTCACTCTGTCCTCGGGCATCAGCTCCCTCGCTGTCATCAT	1755		
257	TGTTTCCAAGGAGGAGTACTTGAGGGATCTACAAAGACTCCACCTGGCTC	Db	1337	TGACGGTCACTCTGTCCTCGGGCATCAGCTCCCTCGCTGTCATCAT	1396		
556	TGTTTCCAAGGAGGAGTACTTGAGGGATCTACAAAGACTCCACCTGGCTC	Qy	1636	GGCGCTGACTCGCAGGCTCTCGCAAGGAGGTGAGGAGGAGGAGGAG	1695		
197	TGTTTCCAAGGAGGAGTACTTGAGGGATCTACAAAGACTCCACCTGGCTC	Db	1397	GGCGCTGACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1456		
496	GGCTGGTAACTCCGGGTGTCCGGCTGGCAGGAGTCTCCGGAGCTTAC	Qy	1756	GAGGACACCCGGTACCGAGGACCTGGGCTGGGTCAG	1755		
377	GGCTGGTAACTCCGGGTGTCCGGCTGGCAGGAGTCTCCGGAGCTTAC	Db	1457	TGACGGTCACTCTGTCCTCGGGCATCAGCTCCCTCGCTGTCATCAT	1516		
676	GGCTGGTAACTCCGGGTGTCCGGCTGGCAGGAGTCTCCGGAGCTTAC	Qy	1756	GAGGACACCCGGTACCGAGGACCTGGGCTGGGTCAG	1755		
437	GGCTGGTAACTCCGGGTGTCCGGCTGGCAGGAGTCTCCGGAGCTTAC	Db	1337	TGACGGTCACTCTGTCCTCGGGCATCAGCTCCCTCGCTGTCATCAT	1396		
736	AGGAGATCTCAGGACATGAGGACCTTGAGGGAGGAGGAGGAGGAGGAG	Qy	1816	GTGCCCCATGGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1875		
497	AGGAGATCTCAGGACATGAGGACCTTGAGGGAGGAGGAGGAGGAGGAG	Db	1577	GTGCCCCATGGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1636		
796	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Qy	1876	CTTACGGCGTCCCTCGAGGAGGCCCTGGGATCGCCCTCTGGGATCT	1935		
617	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Db	1637	CTTACGGCGTCCCTCGAGGAGGCCCTGGGATCTGGGATCTGGGCT	1696		
557	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Qy	1936	ACACCCGGCTACAGGGGGACTATGGAGCTGAGAAGGCCCTGGGCT	1995		
856	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Db	1697	ACACCCGGCTACAGGGGGACTATGGAGCTGAGAAGGCCCTGGGCT	1756		
617	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Qy	1936	ACACCCGGCTACAGGGGGACTATGGAGCTGAGAAGGCCCTGGGCT	1995		
916	GGGAGACATGATTATCTGAGGCGGTGACCTCAACGGTCCACCTAAGACGACATA	Qy	1996	CCACACTTCCCAGAACAGGRCGCCCCATTGGCCGGGTGACATGTTACCTGGAG	2055		
677	GGGAGACATGATTATCTGAGGCGGTGACCTCAACGGTCCACCTAAGACGACATA	Db	1757	CCACACTTCCCAGAACAGGRCGCCCCATTGGCCGGGTGACATGTTACCTGGAG	1816		
976	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Qy	2056	GGTCACGGGGCAACACCTATGGCTCTGGGCTGACCTCCCCGGGCACTGGGGAG	2115		
137	GGGTGCGGAGCTGGTCTCTACCCCGGGCTGACCGGGCTCATGGCTGTC	Db	1817	GGTCACGGGGCAACACCTATGGCTCTGGGCTGACCTCCCCGGGCACTGGGGAG	1876		
1036	ATGACTTGTAGGAGAGTCAGGAGCTGGGGCTGGCCAGGCTATGACTTGAGGATGGA	Qy	2116	GGGGCCAGAGGAGTCCCTGGGCTGACCTCCCCGGGCACTGGGGAG	2175		
179	ATGACTTGTAGGAGAGTCAGGAGCTGGGGCTGGCCAGGCTATGACTTGAGGATGGA	Db	1877	GGGGCCAGAGGAGTCCCTGGGCTGACCTCCCCGGGCACTGGGGAG	1936		
1096	GGACACAGCTCTCCAGTGTGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGG	Qy	2176	GGCGTTGGGGAGGTCACCTGGTGTAGGAGGAGGAGGAGGAGGAGGAGG	2235		
857	GGACACAGCTCTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	Db	1937	GGCGTTGGGGAGGTCACCTGGTGTAGGAGGAGGAGGAGGAGGAGGAGG	1996		
1156	GGGGGGTGAATCTCGCTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG	Qy	2236	ATTCGGCTTATGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2295		
917	GGGGGGTGAATCTCGCTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG	Db	197	ATTCGGCTTATGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2056		
1216	GGGGGGTGAATCTCGCTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG	Qy	2296	CAGATGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2355		
977	GGGGGGTGAATCTCGCTCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG	Db	2057	CAGATGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2098		
1276	GGCACACAACCTAGGGGCCACCTGGGGACCCAGAGGCCGGCTGTCAGGCCCTTG	Qy	2356	TGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2415		

QY	2416	AGGACGACCCCTCTGCAATGATCTGACTACATGAGAACGCGGACCTCACCGATTC	2475	QY	3495	ACACTGGACCCACTTGCTGAGAATCTGGGGTGGAGGACAGAAGGAGGAATG	3554	
Db	2159	AGGAGGACCCCTCTGCAATGATCTGACTACATGAGAACGCGGACCTCACCGATTC	2218	Db	3113	ACACTGGACCCACTTGCTGAGAATCTGGGGTGGAGGACAGAAGGAGGAATG	3212	
QY	2476	TCACTGCCACCCAGCTGGAGAACAGAGGGACCCAGGGGGCCCTGGGACGGGGCAG	2335	QY	3555	TTCTCTTGAGCTGCTCTGACTTGCTCTCAGCTGGCTCTCTCTCTCTCTCACCT	3614	
Db	2219	TCACTGCCACCCAGCTGGAGAACAGAGGGACCCAGGGGGCCCTGGGACGGGGCAG	2278	Db	3213	TTCTCTTGAGCTGCTCTGACTTGCTCTCAGCTGGCTCTCTCTCTCTCACCT	3272	
QY	2536	CGCAGGGGCCACCATCACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCT	2295	QY	3615	GAACACTGACCTGGGGTGGACCCAGCCAGCTGCGCATGTCGCACTGGCTCTCG	3674	
Db	2279	CGCAGGGGCCACCATCACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCT	2338	Db	3273	GAACACTGACCTGGGGTGGACCCAGCCAGCTGCGCATGTCGCACTGGCTCTCG	3332	
QY	2596	GCATGCCATCTGCCACACTAACCTAACCTAACCTAACCTAACCTAACCTAACCT	2655	QY	3675	CAGCTTGAGCTGAGACTCTCTAGCTTACCTTGTGGAGTAATATGGATT	3734	
Db	2339	GCATGCCATCTGCCACACTAACCTAACCTAACCTAACCTAACCTAACCTAACCT	2398	Db	3333	CAGCTTGAGCTGAGACTCTCTAGCTTACATCGGACCTGGCCACGGGAACTGCC	3392	
QY	2656	TAGTGGGGAAATTTCACCATCACATCAAATGCGAACACTTGGCATAGCGAACCT	2715	QY	3735	GGGGGAAAGGGGACAGGCCATACGCCCTGGGTGAGACATCTCTAGTGTAGCTC	3794	
Db	2399	TAGTGGGGAAATTTCACCATCACATCAAATGCGAACACTTGGCATAGCGAACCT	2458	Db	3393	GGGGGAAAGGGGACAGGCCATACGCCCTGGGTGAGACATCTCTAGTGTAGCTC	3452	
QY	2716	CTGGGGACTATTAACCGTGGCAGGGCCAGGCTTGGCAACTCACCGAGGAGCAG	2775	QY	3795	CACATTGATTTCTATACTACTTGGSPTGACATTGGGGAGAGACAGT	3854	
Db	2459	CTGGGGACTATTAACCGTGGCAGGGCCAGGCTTGGCAACTCACCGAGGAGCAG	2518	Db	3453	CACATTGATTTCTATACTACTTGGSPTGACATTGGGGAGAGACAGT	3512	
Db	2579	TGTGGGAAATTTCACCATCACAAATGCGAACACTTGGCAAGCTCACCGAGGAGCAG	2638	QY	3855	TTTACACTATATGACCTACTTGAGGAAATTATCCCTGCACTAGCCAGTA	3914	
QY	2896	TCATCGGAGACGCGGGGGAGTTCCGGACAGGGGGGGGGGGGGGGGGGGGGGGGG	2955	Db	3513	TTTACACTATATGACCTACTTGGSPTGACATTGGGGAGAGACAGT	3572	
Db	2639	TCATCGGAGACGCGGGGGAGTTCCGGACAGGGGGGGGGGGGGGGGGGGGGGGGG	2698	QY	3915	ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA	3953	
Db	2956	CGCCCTGGCCGGCCGGCCAGGGCTATATGAGCTGAGTGGCTGGGACGGAGCTG	3015	Db	3573	ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA	3611	
Db	2699	CGCCCTGGCCGGCCGGCCAGGGCTATATGAGCTGAGTGGCTGGGACGGAGCTG	2758	RESULT	10			
QY	3016	AGCAGGGACACCTTTCCAGGGATCTGCACTGGGCTCTGGCAAGGGATGACTAACAGG	3075	LOCUS	180845			
Db	2759	AGCAGGGACACCTTTCCAGGGATCTGCACTGGGCTCTGGCAAGGGATGACTAACAGG	2818	DEFINITION	Sequence 3 from patent US 5709858.			
QY	3076	TGTGATCATCACATCCAGGCTCTCTGGAGGATGCTGGGAGGCACTGAGCA	3135	ACCESSION	180845			
Db	2819	TGTGATCATCACATCCAGGCTCTCTGGAGGATGCTGGGAGGCACTGAGCA	2878	VERSION	180845.1			
QY	3136	CTAAACAAAGGACACCTTTCCAGGCTCTCTGGAGGATGCTGGGAGGCACTC	3195	KEYWORDS	US 5709858-A 3 20-JAN-1998;			
Db	2879	CTAAACAAAGGACACCTTTCCAGGCTCTCTGGAGGATGCTGGGAGGCACTC	2938	ORGANISM	Unknown.			
QY	3196	ATAGAGGAGGATGAGCTGGAGGGGGGCCCCACCCAGGGAGCTATGCCCTCTC	3255	REFERENCE	1 (bases 1 to 3637)			
Db	2939	ATAGAGGAGGATGAGCTGGAGCTG-----	2958	AUTHORS	Godowski, P.J., Mark, M.R. and Scadden, D.T.			
QY	3256	CCCTCTCTGGACACACTCTCATGAGCCCTCTGGAGGATGCTGGGAGGATGCTGG	3315	TITLE	Antibodies specific for Re receptor protein tyrosine kinase			
Db	2959	-----AGAGCCCTGAG	2972	JOURNAL	Patent: US 5709858-A 3 20-JAN-1998;			
QY	3316	CCACCCAGCTGCTCTGGAGGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3375	FEATURES	Patent: US 5709858-A 3 20-JAN-1998;			
Db	2973	CCACCCAGCTGCTCTGGAGGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3032	source	1. .3637/			
QY	3376	AAAGTGGGAGAATATAGGATAGACATGGGAGCTGGGAGCTGGGAGCTGGGAGCTGG	3435	BASE COUNT	/organism="unknown"			
Db	3033	AAAGTGGGAGAATATAGGATAGACATGGGAGCTGGGAGCTGGGAGCTGGGAGCTGG	3092	ORIGIN	1. .3637/			
QY	3436	ACTGGACACACTGATCTGGAGGGGGCTGGCAGCTCTCTCTCTCTCTCTCTCTCT	3494	Query Match	87.1%; Score 3451; DB 6; Length 3637;			
Db	3093	ACTGGACACACTGATCTGGAGGGGGCTGGCAGCTCTCTCTCTCTCTCTCTCTCT	3152	Best Local Similarity	97.0%; Pred. No. 0;			
QY	3495	ACGGACCATCCCAGACAGCTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3554	Matches	3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;			
Db	3113	ACGGACCATCCCAGACAGCTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3212	QY	256	GTGGACTCTGAGGAATGCGCAAGAGATGCTGGCCCTAGGCCCCCTAGGCCCCAGGGATGAG	315	
Db	3153	ACGGACCATCCCAGACAGCTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3272	Db	17	GTGGACTCTGAGGAATGCGCAAGAGATGCTGGCCCTAGGCCCCCTAGGCCCCAGGGATGAG	76	
QY	3555	TTCTCTTGAGCTGCTCTGACTTGCTCTCAGCTGGCTCTCTCTCTCTCTCTCT	3614	QY	316	GACCTATGGAGGAGGGCCCTCTGAGTGTGCTCTGCTCTGCTCTGGCACTGGAG	375	
Db	3213	TTCTCTTGAGCTGCTCTGACTTGCTCTCAGCTGGCTCTCTCTCTCTCTCTCT	3272	Db	77	GACCTATGGAGGAGGGCCCTCTGAGTGTGCTCTGCTCTGGCACTGGAG	136	
QY	3615	GAACACTGACCTGGGGTGGACCCAGCCAGCTGCGCATGTCGCACTGGCTCTCG	3674	QY	376	ATGCTGACATGAAGGGACATTTGATCTGCTGGCACTGGCTCTGGCACTGGAG	435	
Db	3273	GAACACTGACCTGGGGTGGACCCAGCCAGCTGCGCATGTCGCACTGGCTCTCG	3332	Db	137	ATGCTGACATGAAGGGACATTTGATCTGCTGGCACTGGCTCTGGCACTGGAG	196	
QY	3675	CAGCTTGAGCTGAGACTCTCTAGCTTACCTTGTGGAGTAATATGGATT	3734	QY	436	ACGGACCATCCCAGACAGCTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT	495	
Db	3333	CAGCTTGAGCTGAGACTCTCTAGCTTACCTTGTGGAGTAATATGGATT	3392	Db	197	ACGGACCATCCCAGACAGCTGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT	256	

Qy	496	CCGGCACAGCAGGTTGGAGACAGTACGGGATGGGCCCTGGTACCCSAGGGTGG	555	Qy	1576	TCACTGGCTGCCGGTGCACATCCTGCTCTGCTCATGCCCCTCATGCTT	1635
Db	257	CCGCCACAGCAGGTTGGAGACAGTACGGGATGGGCCCTGGTACCCSAGGGTGG	516	Db	1337	TCACTGGCTGCCGGTGCACATCCTGCTCTGCTCATGCCCCTCATGCTT	1396
Qy	556	TGTTCCAAGGAGGAGGACTCTGAGGTTGGAGACAGTACGGGATGGGCCCTGGTACCCSAGGGTGG	615	Qy	1636	GGGGCTACAGGGAGGCTCTGAGGAGGACTCTGAGGTTGGAGAGGAGG	1695
Db	317	TGTTCCAAGGAGGAGGACTCTGAGGTTGGAGACAGTACGGGATGGGCCCTGGTACCCSAGGGTGG	376	Db	1397	GGGGCTACAGGGAGGCTCTGAGGAGGACTCTGAGGTTGGAGAGGAGG	1456
Qy	616	TGGGGGACCCAGGGGGCAGGGGGCTGGCAAGGAGTCTCCGGAGCTAC	675	Qy	1696	TGAGGTACCTCTGCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1755
Db	377	TGGGGGACCCAGGGGGCTGGCAAGGAGTCTCCGGAGCTAC	436	Db	1457	TGAGGTACCTCTGCTGGGGAGGAGGAGGAGGAGGAGGAGGAGG	1516
Qy	736	AGGTGATCTAGGCAATGAGGCGCTGGGGCTGGAGGAGGAGGAGGAGGAGG	735	Qy	1756	GAGGCCCGGGTACAGGGGGCTGGAGGAGGAGGAGGAGGAGGAGG	1815
Db	497	AGGTGATCTAGGCAATGAGGCGCTGGGGCTGGAGGAGGAGGAGGAGG	556	Db	1517	GAGGCCCGGGTACAGGGAGGAGGAGGAGGAGGAGGAGGAGG	1576
Qy	796	TGTTGCCGAGCTGGTGCCTACACCCGGCTGACCGGGCATGAGTGTGTC	855	Qy	1816	GTCGCCATGCTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGG	1875
Db	557	TGTTGCCGAGCTGGTGCCTACACCCGGCTGACCGGGCATGAGTGTGTC	616	Db	1577	GTCGCCATGCTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGG	1636
Qy	856	GGGTAGCTCTATGGTGCCTCTGGGGATGGACTCTCTCTTACACCCGGCTGG	915	Qy	1876	CITACGCCATGCTCTGGGGAGGAGGAGGAGGAGGAGGAGG	1935
Db	617	GGTAGAGCTCTATGGTGCCTCTGGGGATGGACTCTCTCTTACACCCGGCTGG	676	Db	1537	CITACGCCATGCTCTGGGGAGGAGGAGGAGGAGGAGGAGG	1696
Qy	916	GGCAGACAATGTTATCTGGGGCTGCGCTACGACTCCACTATGAGGACATA	975	Qy	1936	ACACCCAGCCUPACGGGGACTATATGGACCTGAGAACCCAGCCAGCC	1995
Db	677	GGCAGACAATGTTATCTGGGGCTGCGCTACGACTCCACTATGAGGACATA	736	Db	1697	ACACCCAGCCUPACGGGGACTATATGGACCTGAGAACCCAGCCAGCC	1756
Qy	976	CGTGGGGAGCTGAGTATGGGGCTGGGGAGCTGGGGAGGATGGTGGGGCTGG	1035	Qy	1995	CCACACTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2055
Db	737	CGTGGGGAGCTGAGTATGGGGCTGGGGAGCTGGGGAGGAGGAGGAGGAGG	796	Db	1757	CCACACTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1816
Qy	1036	ATGACTTTAGGAGAGCTGGGGCTGGGGCTGGGGAGGATGGGGATGGGA	1095	Qy	2056	GGTCACGGGGCAACACCTATGGCTGGGGAGGAGGAGGAGGAGG	2115
Db	797	ATGACTTTAGGAGAGCTGGGGCTGGGGAGGAGGAGGAGGAGGAGGAGG	856	Db	1817	GGTCACGGGGCAACACCTATGGCTGGGGAGGAGGAGGAGGAGG	1876
Qy	1096	GCACACACGCTTCAGGCTGGCTATGGGGAGGAGGAGGAGGAGGAGG	1155	Qy	2116	GACCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2175
Db	857	GCACACACGCTTCAGGCTGGCTATGGGGAGGAGGAGGAGGAGGAGG	916	Db	1877	GCCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1936
Qy	1156	CCTCAGGCTATGAGTCAGTACGACACATGACACCTGGGGAGGCCATGC	1215	Qy	2176	GCAGTTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2235
Db	917	CCTCAGGCTATGAGTCAGTACGACACATGACACACAGGGCTGGCTGG	976	Db	1937	GCCAGTTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1996
Qy	1216	GGGGGTGGATGTCCTCGGGCTGGGGCTGGGGAGGGGGAGGCCATGC	1275	Qy	2236	ATTCCTCTATGGGGTAGGGACACCTGGGGAGGAGGAGGAGG	2295
Db	977	GGGGGTGGATGTCCTCGGGCTGGGGAGGGGGAGGCCATGC	1036	Db	1997	ATTCCTCTATGGGGTAGGGACACCTGGGGAGGAGGAGGAGG	2056
Qy	1276	GCACACCTGGGGCAACCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCC	1335	Qy	2299	CAGATGCCAACGAAATGCCAGCTCTCTCTCTGGGGAGGAGGAGG	2355
Db	1037	GCACACCTGGGGCAACCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCC	1096	Db	2057	CAGATGCCAACGAAATGCCAGCTCTGGGGAGGAGGAGGAGG	2098
Qy	1336	GCACACCTGGGGCAACCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCC	1395	Qy	2356	TGAGATCTCTGGGGCTCAAGGACCCACATCATCTGGGGAGGAGGAGG	2415
Db	1097	GCACACCTGGGGCAACCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCC	1156	Db	2099	TGAGATCTCTGGGGCTCAAGGACCCACATCATCTGGGGAGGAGGAGG	2158
Qy	1456	CTTCCGGGAGGCCCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	1515	Qy	2476	TGAGTGCACGGGGCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	2535
Db	1217	CTTCCGGGAGGCCCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	1276	Db	2219	TGAGTGCACGGGGCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	2278
Qy	1516	AGCTGGAGCCAGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	1575	Qy	2596	GCATGGCTATCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	2655
Db	1277	AGCTGGAGCCAGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	1336	Db	2339	GCATGGCTATCTGGGGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC	2398
Qy	2656	TAGTGGGAAATTCCACAAATCGCAGACTTGGCATGAGCCGAACTCTATG	2715				

422	GTGCCCCGTGATGGGTGGAGAGACCTGGGTAGAGGATCTAGGGATAG	481
757	ACCCCTGAGGAGCTGGTGTGAAAGACCTGGGCCCCATGGTGGCCACTTACCCCGTCCCCCTCGAG	1896
482	ACCTGAGGGAGTGTGCTGAAAGACCTGGGCCCCATGGTGGCCACTTACCCCGTCCCCCTCGAG	541
Db	1558	-----
Qy	1897	GCCTGGGCCCCCACCCGCGCTGGCAAACCCACCCAGGCTACAGGG
Db	1558	-----
Qy	1957	ACTATATGGAGCCTGAGAAGCCAGGGCCCTGGGGAGACATGTATTATCG
Db	1571	ACTATATGGAGCCTGAGAAGCCAGGGCCCTGGGGAGACATGTATTATCG
Qy	2017	TCCCCCATATGCCAGGCTGACATTTGTTACCCCTGGGGGTACGGGGCACACCT
Db	1631	TCCCCCATATGCCAGGCTGACATTTGTTACCCCTGGGGGTACGGGGCACACCT
Qy	2077	ATGCCTGTGCTGAGCTGGCCAGGGCTGGGGCTGATGAGCTTGGAGAGTCGG
Db	1691	ATGCCTGTGCTGAGCTGGCCAGGGCTGGGGCTGATGAGCTTGGAGAGTCGG
Qy	2137	CTCGATCTGACTCGTCAGGGCAGGGCAGTGGGGCTGAGCACCACAGCTCTCCAGTG
Db	1751	CTCGATCTGACTCGTCAGGGCAGGGCAGTGGGGCTGAGCACCACAGCTCTCCAGTG
Qy	2197	TGTGAGGTGAGCAGCCCTCAAGATCTGCTGAGCTTGATGGGAGCTGGAGCACC
Db	1811	TGTGAGGTGAGCAGCCCTCAAGATCTGCTGAGCTTGATGGGAGCTGGAGCACC
Qy	2257	AGGGACACCTTGTGGTGGAGTCTGTCAGGCTGGGGGTAATGCGCTCC
Db	1871	AGGGACACCTTGTGGTGGAGTCTGTCAGGCTGGGGGTAATGCGCTCC
Qy	2317	GCTCTCTCTGTCAGGAGATATTCCTGAAGATCATGTCAGGGCACC
Db	1928	-----
Qy	2377	AGGACCCACATCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTC
Db	1973	AGGACCCACATCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTC
Qy	2437	TATCTGACTACATGGAAAGGGCACCTCAACAGGTGTTCTGCCCACCTGGAGG
Db	2033	TATCTGACTACATGGAAAGGGCACCTCAACAGGTGTTCTGCCCACCTGGAGG
Qy	2497	ACAGGACGGGGGCCCTGGGGGAGGGGGAGGGGGAGGGGGGACACATGG
Db	2093	ACAGGACGGGGGCCCTGGGGGAGGGGGAGGGGGAGGGGGACACATGG
Qy	2557	ACCCATGTCGTCATGGGAGCCAGATCGCTCGGGCTGGGATCTGGGACAC
Db	2153	ACCCATGTCGTCATGGGAGCCAGATCGCTCGGGCTGGGATCTGGGACAC
Qy	2617	TCACTTGACTCGGAGCTGGCCAGGGGACTGCTGTTGGGAAATTCCCA
Db	2213	TCACTTGACTCGGAGCTGGCCAGGGGACTGCTGTTGGGAAATTCCCA
Qy	2677	TCAATGGAGCTTGGCATGGCCAGGGGACTGCTGTTGGGAAATTCCCA
Db	2273	TCAATGGAGCTTGGCATGGCCAGGGGACTGCTGTTGGGAAATTCCCA
Qy	2737	AGGGCCGGCAGTGTGCTGCCATCGCTGCTGCTGCTGCTGCTGCTGCTG
Db	2393	AGGGCCGGCAGTGTGCTGCCATCGCTGCTGCTGCTGCTGCTGCTGCTG
Qy	2857	GTAGGGCCAGGCCCTGGGAGCTACCCGAGGGCTGGAGGAGCTGGGAGG
Db	2452	GTAGGGCCAGGCCCTGGGAGCTACCCGAGGGCTGGAGGAGCTGGGAGG
Qy	2916	GTAGGGCCAGGCCCTGGGAGCTACCCGAGGGCTGGAGGAGCTGGGAGG
Db	2453	GTAGGGCCAGGCCCTGGGAGCTACCCGAGGGCTGGAGGAGCTGGGAGG

Db	122	TGATCTGCGCAAGTGCCGATGCCGCTATGCCCTGGCATGCCAGGACGGACATCCAGACAGTG	181	
Qy	457	ACATCTCTGCTCCAGCTCTGGTCAGATCCACTGCCGCCACAGGAGTGGAGA	516	
Db	182	ACATCTCTGCTCCAGCTCTGGTCAGATCCACTGCCGCCACAGGAGTGGAGA	241	
Qy	517	GCAGTGACGGGATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	576	
Db	242	GCAGTGACGGGATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	301	
I	Qy	577	ACTTGAGGGATGATCTACAAAGACATCCACCTGGTGCTGGCTGGGACCCAGGGAGG	636
Db	302	ACTTGAGGGATGATCTACAAAGACATCCACCTGGTGCTGGCTGGGACCCAGGGAGG	361	
Qy	637	ATGGGGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	696	
Db	362	ATGGGGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	421	
Qy	697	GTGCGCGCTGGATGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	756	
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Qy	757	ACCTGAGGGAGTGGTGTGAAGGACCTGGGCCCATGGTGGCCGACTG	816	
Db	482	ACCTGAGGGAGTGGTGTGAAGGACCTGGGCCCATGGTGGCCGACTG	541	
Qy	817	TCTACCCCCGGGCTGACCGGGCTGCTGAGTGTCTGCTGGGGTAGAGCTATG	936	
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Qy	877	TCTGAGGAGATGGACTCCCTGCTACACGCCCTGTGGGGCACACAGTAT	936	
Db	602	TCTGAGGAGATGGACTCCCTGCTACACGCCCTGTGGGGCACACAGTAT	661	
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Db	662	AGCCGCTGTACCTAACCAACTCCACCTAACGACATACGGGGACTGAGT	721	
Qy	997	GGGGCTGGCCACCTGCGAGATGTGGTGGGGCTGGATGACTTGGAGAAGT	1056	
Db	722	GGGGCTGGCCACCTGCGAGATGTGGTGGGGCTGGATGACTTGGAGAAGT	781	
Qy	1057	AGCTGCGGGCTGGCCACGCTGCGAGATGTGGTGGGGCTGGATGACTT	1116	
Db	782	AGCTGCGGGCTGGCCACGCTGCGAGATGTGGTGGGGCTGGATGACTT	841	
Qy	1117	GTGATGCGAGATGGACTTGAGTTGAGCTTGAGCTTGAGCTTGAGG	1176	
Db	842	GTGATGCGAGATGGACTTGAGCTTGAGCTTGAGCTTGAGG	901	
Qy	1237	GGGGTGGCCCTGCATGGGCTGGGAGGGGAGGCCATGGCCACACTAGGG	1296	
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Qy	1297	TGGGGACCCAGAGCCCCGGTGTCTGGCCCTGGGCCGCTGGGGGGTGT	1356	
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Qy	1357	TGCACTGCGCTCTCTGGGGGGCCTGGTGTACTCTTCAGCGAATCTCT	1416	
Db	1082	TGCACTGCGCTCTGGGGGGCCTGGTGTACTCTTCAGCGAATCTCT	1141	
Qy	1417	CTGATGCGGTGACAACTTCTCTGGGGGGCCTGGTGTACTCTTCAGCGA	1476	
Db	1142	CTGATGCGGTGACAACTTCTCTGGGGGGCCTGGTGTACTCTTCAGCGA	1201	
Qy	1477	GGCCGCTGGCCACCTCCACCAACTCAGGACCTGGAGCTGGAGCCCAGGG	1536	
Db	1536	GGCCGCTGGCCACCTCCACCAACTCAGGACCTGGAGCTGGAGCCCAGGG	2212	
Db	1202	GGCGCGCTGGCCACCTCCACCAACTCAGGACCTGGAGCTGGAGCCCAGGG	1261	
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Db	1262	AGCCCGCTGGCCAAAGGGAGGCCACCGGCCACATCCCATCGCTGCTGG	1321	
Qy	1597	TCTCCCTGCTCTGCTCATCTATGCCCTCATCTCTGCGCTGCACTGGG	1656	
Db	1322	TCTCCCTGCTCTGCTCATCTATGCCCTCATCTCTGCGCTGCACTGGG	1381	
Qy	1657	TCTCGACAGGGCTGACGGGGCTGGAGAGGAGGCTGACCTTACCTCTG	1716	
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Qy	1717	CTGGGACACTATCTCATCACAAACGCCAGGCTCTAGAGACACCCCGTAC	1776	
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Qy	1777	AGCCGGGGCTGCTGGGAAATCGGCCAACCTCCCTCGTCCCAATGGCT	1836	
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Qy	1837	TGCTGCTCCAACTCAGCTTACCCCTCTCAGGCCACTTACGGG	1896	
Db	1558	-----	1557	
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Qy	1957	ACTATATGGAGCTGAGAACCCACGGCCCGCTCTGCCAACCTCCCAG	2016	
Db	1571	ACTATATGGAGCTGAGAACCCACGGCCCGCTCTGCCAACCTCCCAG	1630	
Qy	2017	TCCCCATATTGCGAGGCTGACATTTGTRACCTCGAGGGTACCGGGCACCT	2076	
Db	1631	TCCCCATATTGCGAGGCTGACATTTGTRACCTCGAGGGTACCGGGCACCT	1690	
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Db	1691	ATGCTGTGCTGACTGCCCCAAGGGAGATGGCCCTGGCCCAAGTGG	1750	
Qy	2137	CTCGATCTGCACTCGCTCAAGGAAACCTGGGAGGGCACTTGGGAGG	2196	
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Qy	2197	TGTGAGGTCGAGGCCCTCAAGATCTGCTGAGTGGCTTAATGTCG	2256	
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Qy	2317	GCTCTCCCTGTCCTCCAGAATCTTCTGAGAGATCTGTCAGTGTAGG	2376	
Db	1928	-----	1972	
Qy	2377	AGGCCCCACATCTCGCTGGGGTGTGCTGGAGGAGATCTGTCAGG	2436	
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Qy	2497	ACAGGGCGGGCCCTGGGAGGCCAGCTGGGAGGCCAGGCTGGGAGG	2556	
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QY	2077	ATGCTGTGCCGACTGCCCCAGGGCAGTCGGCGATGGCCCTCACGGGAGCTGGGAGTGCTTC	2136	Db	3044	GCACCTGCTGCCTTCCTCCCTCCGACGCCATCACCTCATAGGGCAGTGACTGCA	3103
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QY	2137	CTCGATCTCCTACTCGCTCAAGGAGAAGCTGGCAGGGCCAGTTGGGAGTGCTTC	2196	Db	3104	GGTGGCTSGGCCACCCAGGAGCTGGAGCCAGTTGGGGAGTGCA	3163
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QY	2197	TGTGAGGCGACGCCCTCAAGTCTGTCAGCTGTGATTCCCTTAAGTGGCA	2256	Db	3164	TGTCCCTCTGCTTCTCTCTAGAG-CCTCTGCGCCACCCAGCTGGCTCT	3223
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QY	2257	AGGACACCTTGTGGTAGCTGTCAGAGCTACGGCAGATGCCACAGATGCA	2316	Db	3224	GGATGGATCCTCCACCCCTCTAGGCAACCCCTGGGAGGGAAATA	3283
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Db	2264	AGGACCCACATCATCGCTGGCTGGGCTGTGAGAGATCAGTCAGGCTCA	2223	QY	3574	GTACTGTCTCACTGGCTCTCCCTCTCCATACTGAAACACTGGACCTGGG	3633
QY	2437	TTACTGACTACATGGAGAACGGGACCTGACACAGTCTCA3GCCACAGCTGGAG	2496	Db	3464	GTACTGTCTCACTGGCTCTCCCTCTCCATACTGAAACACTGGACCTGGG	3523
Db	2324	TTACTGACTACATGGAGAACGGCACCTCACAGTCTCCATGCCACACTGGAG	2383	QY	3634	TAGCCCGGCCACCCCTAGTCAACCCACTTCACTGAGCTTGACTGAGACT	3693
QY	2497	ACAGGCGACCGAGGGGCCCTGGGAGGGAGGCTGGAGGGCCACCATCAGT	2556	Db	3524	TAGCCCGGCCACCCCTAGTCAACCCACTTCACTGAGCTTGACTGAGACT	3403
Db	2384	ACGAGCGAGGGGCCCTGGGAGGGAGGCTGGAGCTGGAGGGCCACCATCAGT	2443	QY	3694	TCTCTAAGCTATACTGTTCTGGAGTAAATGGGATGGGGAAAGGGAGCA	3753
QY	2557	ACCAATGCGTCATGTCGAGGCCAGATCCTCGGCACTGGCTACACGAC	2516	Db	3584	TCTCTAAGCTATACTGTTCTGGAGTAAATGGGATGGGGAAAGGGAGCA	3643
Db	2444	ACCAATGCGTCATGTCGAGGCCAGATCCTCGGCACTGGCTACACGAC	2503	QY	3754	CGGCCATAGCCTGGGTGAGCATCTCTAGTGTAGGCCACATTGATTCTATA	3813
QY	2617	TCACTTGTACATGGACCTGGCACCGGACTGCTAGTGGGAAATTCACCA	2676	Db	3644	CGGCCATAGCCTGGGTGAGCATCTCTAGTGTAGGCCACATTGATTCTATA	3703
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Db	2564	TCAATGCGAGACTGGCATGAGCCGAAACTCTATGCTGGGACTATACGGTGC	2623	QY	3874	CCTAGCTGGGTTACATTGGGAGAGCACATTTCACATTAAATATGCA	3933
QY	2737	AGGCCGCGCAGGCTGGCCATGAGCCGAAACTCTATGCTGGGACTATACGGTGC	2796	Db	3764	CCTAGCTGGGTTACATTGGGAGAGCACATTTCACATTAAATATGCA	3823
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QY	2797	TCACTGGGACTGAGCTGGCTGGGCTTGTCAGGAGGATGCTGTGCT	2856	Db	3824	CCACAAAAAA 3841	
Db	2684	TCACTGGGACTGAGCTGGCTGGGCTTGTCAGGAGGATGCTGTGCT	2743	RESULT	14		
QY	2857	GTAGGCCGACGCCCTTGGGAGCTCACGACAGCAGTCATCGAGAACGGGGGAGT	2916	HOMOLOG	HOMOLOGA		
Db	2744	GTAGGCCGACGCCCTTGGGAGCTCACGACAGCAGTCATCGAGAACGGGGGAGT	2803	DEFINITION	Homo sapiens	3692 bp	mRNA
QY	2917	TCTTCCGGGACGCCAGGGGGAGCTGGTACCTGTCGCTGGGAGGGCC	2976	ACCESSION	Cak receptor kinase mRNA, complete cds.		
Db	2804	TCTTCCGGGACGCCAGGGGGAGCTGGTACCTGTCGCTGGGAGGGCC	2863	VERSION	L57508 1	GI:110924	
QY	2977	TATATGACTGAGCTGGCTGGGAGCTGGAGCGACCCCTTCC	3036	KEYWORD	receptor kinase		
Db	2864	TATATGACTGAGCTGGCTGGGAGCTGGAGCGACCCCTTCC	2923	SOURCE	Homo sapiens	lung	CDNA to mRNA.
QY	3037	AGTGGCATGGTCTGGAGAGAGATGACTCACCGTGAATCACACAGTC	3096	ORGANISM	Homo sapiens		
Db	2924	AGTGGCATGGTCTGGAGAGATGACTCACCGTGAATCACACAGTC	2983		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
QY	3097	CCCTCCCTGAGGAGGATCCAGGGAGCGCCTGGAGCTAACACAGACATG	3156	REFERENCE	1 (bases 1 to 3692)	Perez J L, Jing S Q, and Wong T W.	
Db	2984	CCCTCCCTGAGGAGGATCCAGGGAGCGCCTGGAGCTAACACAGACATG	3043	AUTHORS	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines		

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Db	482	TGGCTTGTGTCGACAGGACGATGCCGGCTGGCAAGGAGTCTCCCGA	541		
QY	670	GCTACCGGCTGGTACTCCCGGATGTCGCGCGTGTGGCTGAGGAGTCTCCCGA	729		
Db	542	GCTACCGGCTGGTACTCCCGGATGTCGCGCGTGTGGCTGAGGAGTCTCCCGA	601		
QY	730	GTCAGGAGGTGATCTAGGCAATGAG3ACCCAGGAGGAGTGTGAGACCTGGC	789		
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QY	850	GTCTGGGTTAGACTCTATGCTGCTCTGGAGGATGGACTCTCTGCTTACACGCC	909		
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QY	910	CTGTGGGAGACAATGATTATCAGGGCTGTACTCACAGCTCCACCTATGAGC	969		
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QY	970	GACATCCGGTGGCGACTGCACTGGAGATGGCTGGGGCTGGCCAGCTGGTGG	1029		
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QY	1030	GGCTGATGACTTGTGAGTCAAGGACTGGAGCTGGGCTGGCCAGCTGGTGG	1089		
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QY	1090	GATGGAGCAACACAGCTCTCCAGTGCTGAGATGGATGTTGAGTTGACCGC	1149		
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QY	1150	TGAGGCTCTTCAGGCTATGAGGTCACTGTACACACATGACAGCTGGAGCCGTC	1209		
Db	1022	TGAGGCTCTTCAGGCTATGAGGTCACTGTACACACATGACAGCTGGAGCCGTC	1081		
QY	1210	TGCCGGGGGGTGGATGGCTCGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	1269		
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QY	1270	CCATGCCACACCTAGGGGCAACCTGGGGACOCCAGGCCGGCTCTCAGTC	1329		
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QY	1330	CCCTTGCGCGCGTGTGGCTCTCTGAGTGGCTCTCTGAGTGGCTCTCTGAGTC	1389		
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QY	1390	TACCTCTCAGGAATCTCCCTCATCTCTGATGCTGACAACTCTCCGCGACTG	1449		
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QY	1450	GAGGACCTCCGGCGAGCCCTGGGGCCCTGGGGCCCTGGGGCCACCTCCACACTGAGCA	1509		
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QY	1510	GCTTGAGCTGGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAG	1569		
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QY	1630	TGCTCTGGCGCTGACTGGCCAGGGAGGAGTACTTCAGGGATCTACACGACTCACCTGG	1689		

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Qy	3450	ATTCCTGAGAGGTGCTGCCCCACCTCTCTCCTGACACACTGGACCCACT	3509	
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Qy	3743	AGAGGGCAAGGCCCATAGCTGGGTTGACATCTTAGTGTAGCTGACATG	3802	
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Db	3487	TTTTCTATATCTACCGGGTTGACATT-----GGGGAGAGACAGAGTTA	3546	
Qy	3860	CACTATATGGACCTAGCTGAGCAATTAACTCCCTGCACTAGGAGGTTAAT	3919	
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